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seq_1.html : /S1/S2/gv-data/geneset/geneset/NA2000.DAT:AAA95105
seq_documentation_block :
ID AAA95105 standard; DNA: 1368 BP.
XX AC AAA95105;
XX AG
XX TGT 12-JAN-2001 (first entry)
XX DE Human TNFR1 coding sequence.
XX KW TNFR1; tumour necrosis factor receptor; polymorphism; human
KW tumour; cancer; apoptosis; bacterial infection; ds.
XX OS Homo sapiens.
XX

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|                        |  |                |
|------------------------|--|----------------|
| 291                    | Aasvalle7sg3-7:the21kappaSer17ThrValLeuSerLeuLeuVa | 217            |
| 769                    | AATGTAAGGGCAATGAGGACTACGCAAGAGCTGAGGCGCCGGT        | 818            |
| 217                    | luciferinCly                                       | 234            |
| 819                    | CATTTCCTGCTTGATTTGATCCCTCTTCTGTTAATGT              | 668            |
| 234                    | YFargYrgInArtpLysSerLysCysSerLysCysCysLys          | 250            |
| 869                    | AIGCTTACACGGAACTAACATGACTCCATTGTTGGAAA             | 918            |
| 251                    | serThrProValIleGlySerSerSerSerSerSerSerSerSerSer   | 267            |
| 919                    | TGGCAACGTTAAATAATGGGAACTTGGGAACTTGGGAACTTGGGAA     | 908            |
| 267                    | uAlaArgAsPProSerSerSerSerSerSerSerSerSerSerSer     | 284            |
| 969                    | GSCCGAAAACGAAAGGTTATGTTTATGTTTATGTTTATGTTTATG      | 101            |
| 284                    | LysSerSerProSerSerSerSerSerSerSerSerSerSerSer      | 300            |
| 1014                   | GCCTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG           | 106            |
| 301                    | ProGlyAspLysProAsnPhiAlaLysProArgGluValDalaProPro  | 317            |
| 1069                   | CCCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG        | 111            |
| 317                    | OYVChGChGAlaAspSerSerSerSerSerSerSerSerSerSer      | 331            |
| 1119                   | CTATAGGGGAACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT        | 116            |
| 334                    | LysProAsnSerLysSerSerSerSerSerSerSerSerSerSer      | 350            |
| 1169                   | TCCCCAACCGCTTCATAAACGGGAACTGAGCTGAGCTGAGCT         | 121            |
| 351                    | LysAspAspHisAspSerProAlaThreonUraLysAlaSerAspPhe   | 367            |
| 1219                   | CTAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT        | 126            |
| 367                    | GlySerSerAspLysSerSerSerSerSerSerSerSerSerSer      | 384            |
| 1264                   | ProGlySerSerSerSerSerSerSerSerSerSerSerSerSer      | 311            |
| 384                    | IULICASPGIPLGIGLIGLUGIAGIAGIAGIAGIAGIAGIAGIAGIAGI  | 400            |
| 1319                   | AGATGAACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT       | 136            |
| 401                    | TyrSerMetLeuIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaI  | 417            |
| 1369                   | TACAGATGCTGGCACTGGGACCTGGAGGGGGGGGGGGGGGGGGGG      | 141            |
| 417                    | ArgGluIleGlyArgValLeuArgAspMetAspLeuLeuGlyCysI     | 434            |
| 1419                   | CTGAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT      | 146            |
| 434                    | cGluAspIleGluGluAlaIleCysCysIProAlaAlaIleCysAla    | 450            |
| 1469                   | GGGAGCTACATGAGAAGGCTTCTGCGGCGGGGGGGGGGGGGGGGG      | 151            |
| 451                    | ProSerLeuLeuAla                                    | 455            |
| 1519                   | CCGAGCTCTCAGA                                      | 1533           |
| 4_name:                | 4_AAS2_52_39444_499991_49999_P1A1654               | AA...GATTC     |
| 4_documentation_block: |  |                |
| AAZ09170;              | AAZ09170 standard                                  | CDNA: 2111 BP. |
| 18-Oct-1999            | (first entry)                                      |                |

`qq_documentation_block:`

AAZ05170 standard; cDNA;

0020081704

AAH.0311/U;

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alignment_scores:
    Quality: 24.87 .00
    Partic.: 5.44 .00
    Percent_Similarity: 100.000

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OS Homo sapiens.  
 XX Location/Qualifiers  
 PH K0Y 256 1623  
 PT CDS /  
 PT /  
 PT misc\_signal 2143 . 2149  
 PT misc\_signal 2143 . 2149  
 PT /  
 PT /  
 XX AAU75742-A.  
 XX 04-MAY-1995.  
 DF 11-OCT-1994; 94AU-0075742.  
 XX 12-OCT-1993; 93AU-0107268.  
 XX (YEDA ) YEDA RES & DEV CO LTD.  
 PA Hatkin M., Brakbusch C., Vartolomey E., Wallach D;  
 XX WPI: 1995-194 34/2/26.  
 DR P PSPR: AA875084.  
 XX PT New protease capable of cleaving soluble tumor necrosis factor (TNF) receptor - from cell bound TNF receptor, useful for antagonising deleterious effects of TNF.  
 XX Disclosure; fig 1. 40pp. English.  
 XX CC This sequence represents human p55 tumour necrosis factor (TNF-R) DNA. Expression of this receptor is regulated by shedding of the extracellular receptor fragment, the p55 TNF-R can be shed in response to different inducing agents e.g. phorbol myristate acetate (PMA), depending on cell type. The only region of the receptor whose structure affects the shedding response is the spacer region (see AR75012) in the extracellular domain. This region is located close to a site of cleavage of the molecule, and links the Cys rich module to the transmembrane domain. The spacer region of the isolated receptor was used to create the chimeras between human p55 TNF-R and murine epidermal growth factor receptor (EGF-R) that are represented by AR75007-11. This spacer region was subjected to deletion mutations (AR75013-25) and substitutions (AR75026-47) of the spacer region, the most important residues are Asn 172, Val 173, Iys 174 and Gly 175, with Val 173 being the most important of these. The shedding of the receptor is independent of the side chain identity of these residues, with the exception of a limited dependence on the identity of Val 173. Mutations which alter the conformation of the protein adversely effect the shedding process. The mutations shown in AR75013-47 were introduced in order to create an inhibitor of a protease that is capable of cleaving the soluble TNF-R from the cell bound TNF-R. Fragments of these inhibitors can be seen in AR75017-9, AR85025, AR8503-5 and AR75042-3. These protease inhibitors can be used to enhance TNF function.  
 XX Sequence 2176 RP: 474 A: 642 C: 603 G: 456 T: 0 other:  
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 Ratio: 5.466 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000  
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 1 MetGlyLeuSerThrValProAspLeuIleProLeuValLeuGu 17  
 256 ALGGAGTCCTGATTCATGGAGCAGTCGTCGGCGTGTCCGGA 305  
 317 tyrcinglyAlaAspProLeuAlaThrAlaLeuAlaSerAspProI 334

|  |   |               |
|--|---|---------------|
| 1206   | CTTAACTGTTATTAATTTTAACTTCAACCTTCAGTCAATAATAA          | 1255          |
| 334  | IeProAsnProLeuGlnIystPheLaspSerAlaHisIysProGlnSer     | 350           |
| 1256   | TCGCCAACCCCTCACAGGCGGAAACAGCAGAACACAGAACGAC           | 1305          |
| 351  | LewAspThrAspPheProAlaThrLeuTyralaValValGlyAlaValPhe   | 367           |
| 1306   | CTGACACTGATACCCCGAGCTGAGCTGAGCTGAGCTGAGCTGAG          | 1355          |
| 367  | oproleuargirpylestaphylvalArgArgGlnQ7conGtaASPHE      | 484           |
| 1356   | QGCTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG          | 1405          |
| 384  | IuLleAspArgIeuGluGlnAsnGlyIArgCystLeuGlnGluAlaGln     | 400           |
| 1406   | AGATGCAATGCCCTGGAGGCAAGGCAACCGCGGCGCTGGAGGGCAA        | 1455          |
| 401  | TYRSerMetLeuAlaThrIeuGlnAsnGlyIArgCystLeuGlnGluAlaGln | 417           |
| 1456   | IACGAACTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG        | 505           |
| 417  | fleuGluGluLeuGlyAla9ValIeuAlaGluPheLeuGlyCysI         | 434           |
| 1506   | GTTGAGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAG         | 555           |
| 434  | eugluAspIleGluGlnIeuGlyCystPheAlaIeuProAlaAla         | 450           |
| 1556   | IGGAGGACATGGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCG           | 605           |
| 451  | ProserLeuLeuIeuG                                      | 455           |
| 1606   | CCAGCTCTCTACA   | 1626          |
| q_value: /Sisus2/j-gstat/gprotein_sensitivity/NA1q001/NA1q001_qc_documentation.html<br>AAQ10955 standard; cDNA; 2111 BP. |   |               |
| AAQ10955;  |   |               |
| 24   | -MAY-1991 (first entry)                               |               |
| Encodes human 55kD TNF-binding protein.  |   |               |
| Tumour Necrosis Factor, binding protein, septic shock; autoimmune glomerulonephritis; lymphokine; cytokine.              |   |               |
| Key  |   |               |
| sig_peptide  | 187...273   |               |
| mat_peptide  | /tag-<br>/tag-<br>/product- 55kD TNF-BP               |               |
| EP417563-A.  |   |               |
| 20   | -MAR-1991.  |               |
| 31   | -Ami-1990:  | 90EP-0116707. |
| 20   | -APR-1990:  | 90CH-0001347. |
| 12   | -SEP-1989:  | 89CH-0003319. |
| 08   | -MAR-1990:  | 90CH-0000746. |
| (HOFF ) HOFFMANN-LA ROCHE AG.  |   |               |
| Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H, Schlaeger EJ;   |   |               |
| WPI: 1991-081951/2.<br>P-PSDB: AAR11082.   |   |               |



|      | 356  | TAGTCACATGGGAAAGAGAGATGTGTGTCCTAGGAAATTATATC | 405 |
|------|--|--|-----|
| 51   | HISPROGLNAsnSerIleCysCysthrValSerIleCysLysIleThr     | 67   |     |
|      |  |  |     |
| 406  | CACCCCAAAATAAAGCAACAA                                | 455  |     |
| 67   | rLeuIrrAspCysProGlyPheGlnAspThrAspCysSerGluC         | 84   |     |
|      |  |  |     |
| 456  | GTCGAAATGACTGTTTCCAGGCTTGAGAACCTGGAGGAGI             | 505  |     |
| 84   | YSGLUSerCysSerDhrAlaSerGluAsnHisSerDhrHisCysL        | 100  |     |
|      |  |  |     |
| 506  | GTGAGGCGGCCTTCATGGCTTAGAAAATGCCAGAAGCTGACTG          | 555  |     |
| 101  | SerCysSerCysSerArgSerGlyMetCysValSerSerCys           | 117  |     |
|      |  |  |     |
| 556  | AGCTGTCUCAAATGCCGAAAGAAATGGGTCAAGGAGATCUC            | 605  |     |
| 117  | stRNA1AspArgAspThrValCysSerArgLysSerGlnTyrPheR       | 134  |     |
|      |  |  |     |
| 606  | CACACGGACGGATACCGIGGGCAGCAGAACCCACACCGC              | 555  |     |
| 134  | ISYTFTRPSerGluAsnLeuPheGlnCysProAspCysSerLeuCysLeu   | 150  |     |
|      |  |  |     |
| 656  | ATTATGGATGAAACATTGTTCTAGTGTGTTATTTGGAGTCGTC          | 705  |     |
| 151  | AsnGlyThrValHistSerCysDlgluLysLnsnThrValCysThr       | 167  |     |
|      |  |  |     |
| 706  | AAGGUSACCGGACGACCCGACGACGACGACGACGACGACGAC           | 755  |     |
| 167  | rcysHsMslaglyPheLeuArgLysValSerCysSerCysSer          | 184  |     |
|      |  |  |     |
| 756  | CTGGCAAGGAGTCTCTCTCTAAAGAAAACGACGCTGCTGCTA           | 805  |     |
| 184  | sncysLysTssCysCysSerCysSerCysSerCysSerCysSer         | 200  |     |
|      |  |  |     |
| 806  | AGTGAGAAAAGGTGCTATTAAGAATTTTATGATGATGATGAG           | 856  |     |
| 201  | AsnValLysSerCysSerCysSerCysSerCysSerCysSerCys        | 217  |     |
|      |  |  |     |
| 856  | AATGTTAAAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC             | 905  |     |
| 217  | LleDphPheGlnLysLeuAspSerLeuAspPheLysLeuDp            | 234  |     |
|      |  |  |     |
| 906  | CATTTCCTGGCTTCTGGCTTAAUCCCTCCUCCATGGTTAAAGT          | 955  |     |
| 234  | YRATGTCInargTCysSerLysSerLysSerLysSerLysSer          | 250  |     |
|      |  |  |     |
| 956  | ATGTTTAAAGGTTAAATGTTAAATGTTAAATGTTAAATGTTAA          | 1000   |     |
| 251  | SerThrProGlnSerCysSerCysSerCysSerCysSerCysSer        | 267  |     |
|      |  |  |     |
| 1006 | TCGACCGAAAGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG           | 1055   |     |
| 267  | dAlaProAspProSerPheSerCysSerCysSerCysSerCysSer       | 284  |     |
|      |  |  |     |
| 1056 | GCCTCCAAACCAAAACCAAAACCAAAACCAAAACCAAAAC             | 1100   |     |
| 284  | LysSerSerValProGlySerLysSerSerSerSerSerSerSer        | 317  |     |
|      |  |  |     |
| 1106 | GCTTGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC             | 1155   |     |
| 301  | PROGLYASpCysProAspHeAlaAlaProArgGluValAlaPro         | 317  |     |
|      |  |  |     |
| 1156 | GGGGTCAATGTCCTCAACTGGGCTCCTGGGAGAGGGTGACACC          | 1205   |     |
| 317  | GlyArgLysValAspSerPheAlaAlaSerAspSerPro              | 334  |     |
|      |  |  |     |
| 1206 | CTACGGGCGCTGACCCATCTGGACACGCTGCTGGGACGCCA            | 1255   |     |
| 334  | LepProAsnProLeuGlnLysItpGluAspSerAlaHistylsProGlnSer | 350  |     |
|      |  |  |     |
| 1256 | TCTTAACGCTTAAATGAAAGAAATAGAAATGAAATGAAATGAA          | 1300   |     |







|                          |  |      |    |  |
|--------------------------|--|------|----|--|
| 117                      | sibrvalaspargasphrvalcysctycysaralysaspoIntyArch       | 134  | XX | Rat tumour Necrosis Factor receptor & cDNA.                |
| 563                      | CAGTGAACTGGAAACCTTCTACTGAGAGAACATACGGC                 | 612  | DE | TRF Receptor   |
| 134                      | istyriferSerGluAspIleAspGlypheAspCysSerIleCyste        | 150  | XX | Tumour Necrosis Factor binding Protein, TRF, TRF-receptor; |
| 613                      | ATTATGGAGGAAACCTTCAGGCTCAANTGACGCCCTGCCTC              | 662  | KW | ratTNF-RB; ss.   |
| 151                      | AspIleTyrrValHistIleSerCysSlnGlyysDlnAspThrValCyst     | 167  | KW | ratTNF-RB; ss.   |
| 663                      | AATGGAArrGrrGrrGrrGrrGrrGrrGrrGrrGrrGrrGrrGrrG         | 712  | XX | Rat ratus.   |
| 167                      | rcysHisAlaClyphebetaArgGluAspClyysValSerCysSerA        | 184  | OS | Localization/Qualities                                     |
| 713                      | CTGCATCGAGTTCTCTANGAGAAAAGGATTTGTCCCTNTA               | 762  | FH |  |
| 184                      | serCysSerSerIleGlySerIleCysSerIleCysSerIleCys          | 290  | FT |  |
| 763                      | ACTGAAATAAAACCCGAGCAGCAACAGGAGCAACACCGTGTGCA           | 812  | CE |  |
| 201                      | AsnValIlysGlyIleGlySerIleSerGlySerIleSerGlySerIle      | 217  | FT |  |
| 813                      | AACTTAAGGAACTGAGAACAGCAGGACACAGCTGCTGCGCTGG            | 862  | FT |  |
| 217                      | IleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle | 234  | PR |  |
| 863                      | CATTCCTGGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTAAT          | 912  | PR |  |
| 234                      | YIARGTCIICAIIGTIGTIGTIGTIGTIGTIGTIGTIGTIGTIGTIG        | 250  | DR |  |
| 913                      | ATGCTACCACACGCGGAAAGCAGCAAGCTTACCCATGTTGCGCAA          | 962  | PR |  |
| 251                      | SerThrPheGlySerIleSerIleSerIleSerIleSerIleSerIle       | 267  | PA | (BOEH ) BOEHRINGER INGELHEIM INT.                          |
| 963                      | ICGACACTGAAAAGACGGAAAGCTGAAGAAACTACTAAGCCCC            | 1012 | XX |  |
| 267                      | ValIapCysPro-Ser-Pro-Pro-PhePro-PhePro-PheProLeu       | 284  | PA | Hauptmann R, Himmer A, Maurer-Fogy I, Stratakis C;         |
| 1013                     | GCGGCCGCGCCAGCTTTCAGCTTTCAGCTTTCAGCTTTCAGCT            | 1062 | PT |  |
| 284                      | LysPheSerIleSerValProSerSerIleSerSerIleSerSerIle       | 300  | PR |  |
| 1063                     | GCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG               | 1112 | PS |  |
| 301                      | ProGlyAspCysSerGlnAspAlaProGlnAspAlaProGlnAsp          | 317  | PS |  |
| 1113                     | CCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG               | 1162 | PS |  |
| 317                      | CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG             | 334  | PS |  |
| 1113                     | CTCATACAGCTTACCATGCTTACCATGCTTACCATGCTTACCAT           | 1212 | PS |  |
| 334                      | IleProAspIleProGluGlyIleIleIleIleIleIleIleIleIleIle    | 350  | PS |  |
| 1213                     | CCGCAACGCCCTCACACACACACACACACACACACACACAC              | 1262 | PS |  |
| 351                      | LeuAspThrAspSerProAlaIleSerIleSerIleSerIleSerIle       | 367  | PS |  |
| 1263                     | CTAGACATGATGACCTGGACGCTAACCCCTGGGCTGAACTGTC            | 1312 | PS |  |
| 367                      | opoleUArgTyrypIleGlyIleGlyIleGlyIleGlyIleGlyIle        | 474  | PS |  |
| 1313                     | CTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT            | 1334 | PS |  |
| seq_name:                | seq_09-525-998a-2_fasta                                | 1334 | PS |  |
| seq_documentation_block: | first  | 1334 | PS |  |
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| XX                       |  | 1334 | PS |  |
| AC                       |  | 1334 | PS |  |
| XX                       |  | 1334 | PS |  |
| DD                       | 29-JAN-1991 ( first entry)                             | 1334 | PS |  |





